

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Quertermous, Thomas
Hogan, Brigid
Snodgrass, H. Ralph
Zupancic, Thomas J.
- (ii) TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
CELL LOCUS-1
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: 05-JUN-1996
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Poissant, Brian M.
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-034
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15

Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
 20 25 30
 Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
 35 40 45
 Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
 50 55 60
 Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
 65 70 75 80
 Leu Pro Leu Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val
 20 25 30
 Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
 35 40 45
 Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
 50 55 60
 Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
 65 70 75 80
 Leu Pro Val Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Cys Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile
 20 25 30
 His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
 35 40 45
 Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
 50 55 60
 Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val
 65 70 75 80
 Ile Pro Lys Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Val Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile
 20 25 30
 Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
 35 40 45
 Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
 50 55 60
 Met Met Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
1 5 10 15
Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
20 25 30
Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
35 40 45
Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
50 55 60
Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
65 70 75 80
Arg Pro Val Thr Trp
85

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Xaa
1 5 10 15
Xaa Gly Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile
20 25 30
Gly Tyr Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser
35 40 45
Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
50 55 60
Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
65 70 75 80
Ile Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Xaa
1 5 10 15
Xaa Xaa Arg Gly Xaa Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile
20 25 30
Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Glu
35 40 45
Tyr Arg Asn Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
50 55 60
Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
65 70 75 80
His Pro Leu Thr Xaa
85

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Leu Xaa Xaa Xaa Xaa Xaa Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15
Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile
20 25 30
Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
50 55 60
Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
65 70 75 80
Xaa Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 619..2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAGTG ATATTTGATT TCCATTCTCA	60
TTCCCAGTGG CCTTGATATT TAAACTGATT CCTGCCACCA GGTCCCTGGG CCACCCTGTC	120
CCTGCGTCTC ATATTTCTGC ATGCTGCTTT GTTTGTATAT AGTGCGCTCC TGGCCTCAGG	180
CTCGCTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCCC GCATCCGCCG	240
CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TGCCTGCGCG CACGGAAATC	300
GGGGAGCCAG GAACCCAAGG AGCCGCCGTC CGCCCGCTGT GCCTCTGCTA GACCACTCGC	360
AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG	420
TGAGGGTGAA TCACCCTTTC TCTAGGGCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTG	480
AGAAGCGCTG CGGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGGCGGGG TTTACTGCTG	540
TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCC GGACCA GCCCAGGTCA	600
CGTCCGTGAG AAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT	651
Met Lys His Leu Val Ala Ala Trp Leu Leu Val	
1 5 10	
GGA CTC AGC CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC	699
Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn	
15 20 25	
CCG AAC CCC TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT	747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp	
30 35 40	
GAT TCC TTT TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC	795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys	
45 50 55	
TCT AGT GTT GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA	843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala	
60 65 70 75	
GGT CCC TGC ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA	891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile	
80 85 90	
AGC GAA GCC TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT	939
Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys	
95 100 105	
CCT CGG GGA TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT	987
Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys	
110 115 120	
GAA GCT GAG CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT	1035

Glu	Ala	Glu	Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala		
125						130					135						
AAC	TAC	TCT	TGT	GAA	TGC	CCA	GGA	GAA	TTT	ATG	GGA	CGA	AAT	TGT	CAA	1083	
Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln		
140					145					150					155		
TAT	AAA	TGC	TCT	GGG	CAC	TTG	GGA	ATC	GAA	GGT	GGG	ATC	ATA	TCT	AAT	1131	
Tyr	Lys	Cys	Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn		
				160					165					170			
CAG	CAA	ATC	ACA	GCT	TCA	TCT	AAT	CAC	CGA	GCT	CTT	TTT	GGA	CTC	CAG	1179	
Gln	Gln	Ile	Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln		
			175					180					185				
AAG	TGG	TAT	CCC	TAC	TAT	GCT	CGA	CTT	AAT	AAG	AAG	GGC	CTT	ATA	AAT	1227	
Lys	Trp	Tyr	Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn		
		190					195					200					
GCC	TGG	ACA	GCT	GCT	GAA	AAT	GAC	AGA	TGG	CCA	TGG	ATT	CAG	ATA	AAT	1275	
Ala	Trp	Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Ile	Asn		
	205					210					215						
TTG	CAA	AGA	AAA	ATG	AGA	GTC	ACT	GGT	GTT	ATT	ACC	CAA	GGA	GCA	AAA	1323	
Leu	Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys		
220					225					230					235		
AGG	ATT	GGA	AGC	CCA	GAG	TAC	ATA	AAA	TCC	TAC	AAA	ATT	GCC	TAC	AGC	1371	
Arg	Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Ser	Tyr	Lys	Ile	Ala	Tyr	Ser		
				240					245					250			
AAT	GAC	GGG	AAG	ACC	TGG	GCA	ATG	TAC	AAA	GTA	AAA	GGC	ACC	AAT	GAA	1419	
Asn	Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu		
			255					260				265					
GAG	ATG	GTC	TTT	CGT	GGA	AAT	GTT	GAT	AAC	AAC	ACA	CCA	TAT	GCT	AAT	1467	
Glu	Met	Val	Phe	Arg	Gly	Asn	Val	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn		
		270					275					280					
TCT	TTC	ACA	CCC	CCA	ATC	AAA	GCT	CAG	TAT	GTA	AGA	CTC	TAC	CCC	CAA	1515	
Ser	Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln		
	285					290					295						
ATT	TGT	CGA	AGG	CAT	TGT	ACT	TTA	AGA	ATG	GAA	CTT	CTT	GGC	TGT	GAG	1563	
Ile	Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu		
300					305					310					315		
CTC	TCA	GGC	TGT	TCA	GAA	CCT	TTG	GGG	ATG	AAA	TCA	GGG	CAT	ATA	CAA	1611	
Leu	Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln		
				320					325					330			
GAC	TAC	CAG	ATC	ACT	GCC	TCC	AGC	GTC	TTC	AGA	ACA	CTC	AAC	ATG	GAC	1659	
Asp	Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Val	Phe	Arg	Thr	Leu	Asn	Met	Asp		
				335				340					345				
ATG	TTT	ACT	TGG	GAA	CCA	AGG	AAA	GCC	AGG	CTG	GAC	AAG	CAA	GGC	AAA	1707	
Met	Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys		
		350					355					360					
GTA	AAT	GCC	TGG	ACT	TCC	GGC	CAT	AAC	GAC	CAG	TCA	CAA	TGG	TTA	CAG	1755	
Val	Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln		
	365					370					375						

GTT GAT CTT CTT GTC CCT ACT AAG GTG ACA GGC ATC ATT ACA CAA GGA	1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly	
380 385 390 395	
GCT AAA GAT TTT GGT CAC GTG CAG TTT GTT GGG TCA TAC AAA CTA GCT	1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala	
400 405 410	
TAC AGC AAT GAT GGA GAA CAC TGG ATG GTG CAC CAG GAT GAA AAA CAG	1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln	
415 420 425	
AGG AAA GAC AAG GTT TTT CAA GGC AAT TTT GAC AAT GAC ACT CAC AGG	1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg	
430 435 440	
AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA TTC ATA AGA ATC CTT	1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu	
445 450 455	
CCT TGG TCC TGG TAT GGA AGG ATC ACT CTG CGG TCA GAG CTG CTG GGC	2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly	
460 465 470 475	
TGC GCA GAG GAG GAA TGAAGTGCGG GGCCGCACAT CCCACAATGC TTTTCTTTAT	2098
Cys Ala Glu Glu Glu	
480	
TTTCCTATAA GTATCTCCAC GAAATGAACT GTGTGAAGCT GATGGAAACT GCATTTGTTT	2158
TTTTCAAAGT GTTCAAATTA TGGTAGGCTA CTGACTGTCT TTTTAGGAGT TCTAAGCTTG	2218
CCTTTTAAAT AATTTAATTT GGTTTCCTTT GCTCAACTCT CTTATGTAAT ATCACACTGT	2278
CTGTGAGTTA CTCTTCTTGT TCTCT	2303

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly	
1 5 10 15	
Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu	
20 25 30	
Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys	
35 40 45	
Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu	
50 55 60	
Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro	
65 70 75 80	

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 85 90 95
 Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
 100 105 110
 Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
 115 120 125
 Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 130 135 140
 Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 145 150 155 160
 His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 165 170 175
 Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 180 185 190
 Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
 195 200 205
 Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
 210 215 220
 Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
 225 230 235 240
 Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
 245 250 255
 Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
 260 265 270
 Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
 275 280 285
 Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
 290 295 300
 Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
 305 310 315 320
 Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
 325 330 335
 Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
 340 345 350
 Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
 355 360 365
 Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
 370 375 380
 Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
 385 390 395 400
 His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
 405 410 415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445

Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460

Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCT	CTT	TAG	TCA	CCA	CTC	TCG	CCC	TCT	CCA	AGA	ATT	TGT	TTA	ACA	AAG	48
Ser	Leu	*	Ser	Pro	Leu	Ser	Pro	Ser	Pro	Arg	Ile	Cys	Leu	Thr	Lys	
1				5					10					15		
CGC	TGA	GGA	AAG	AGA	ACG	TCT	TCT	TGA	ATT	CTT	TAG	TAG	GGG	CGG	AGT	96
Arg	*	Gly	Lys	Arg	Thr	Ser	Ser	*	Ile	Leu	*	*	Gly	Arg	Ser	
			20					25					30			
CTG	CTG	CTG	CCC	TGC	GCT	GCC	ACC	TCG	GCT	ACA	CTG	CCC	TCC	GCG	ACG	144
Leu	Leu	Leu	Pro	Cys	Ala	Ala	Thr	Ser	Ala	Thr	Leu	Pro	Ser	Ala	Thr	
			35				40					45				
ACC	CCT	GAC	CAG	CCG	GGG	TCA	CGT	CCG	GGA	GAC	GGG	ATC	ATG	AAG	CGC	192
Thr	Pro	Asp	Gln	Pro	Gly	Ser	Arg	Pro	Gly	Asp	Gly	Ile	Met	Lys	Arg	
	50					55					60					
TCG	GTA	GCC	GTC	TGG	CTC	TTG	GTC	GGG	CTC	AGC	CTC	GGT	GTC	CCC	CAG	240
Ser	Val	Ala	Val	Trp	Leu	Leu	Val	Gly	Leu	Ser	Leu	Gly	Val	Pro	Gln	
65				70				75						80		
TTC	GGC	AAA	GGT	GAT	ATT	TGT	GAT	CCC	AAT	CCA	TGT	GAA	AAT	GGA	GGT	288
Phe	Gly	Lys	Gly	Asp	Ile	Cys	Asp	Pro	Asn	Pro	Cys	Glu	Asn	Gly	Gly	
			85					90						95		
ATC	TGT	TTG	CCA	GGA	TTG	GCT	GTA	GGT	TCC	TTT	TCC	TGT	GAG	TGT	CCA	336
Ile	Cys	Leu	Pro	Gly	Leu	Ala	Val	Gly	Ser	Phe	Ser	Cys	Glu	Cys	Pro	
			100					105					110			
GAT	GGC	TTC	ACA	GAC	CCC	AAC	TGT	TCT	AGT	GTT	GTG	GAG	GTT	GCA	TCA	384
Asp	Gly	Phe	Thr	Asp	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu	Val	Ala	Ser	
		115					120					125				

GAT	GAA	GAA	GAA	CCA	ACT	TCA	GCA	GGT	CCC	TGC	ACT	CCT	AAT	CCA	TGC	432
Asp	Glu	Glu	Glu	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Thr	Pro	Asn	Pro	Cys	
	130					135					140					
CAT	AAT	GGA	GGA	ACC	TGT	GAA	ATA	AGT	GAA	GCA	TAC	CGA	GGG	GAT	ACA	480
His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg	Gly	Asp	Thr	
	145				150					155					160	
TTC	ATA	GGC	TAT	GTT	TGT	AAA	TGT	CCC	CGA	GGA	TTT	AAT	GGG	ATT	CAC	528
Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn	Gly	Ile	His	
				165					170					175		
TGT	CAG	CAC	AAC	ATA	AAT	GAA	TGC	GAA	GTT	GAG	CCT	TGC	AAA	AAT	GGT	576
Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Val	Glu	Pro	Cys	Lys	Asn	Gly	
			180					185					190			
GGA	ATA	TGT	ACA	GAT	CTT	GTT	GCT	AAC	TAT	TCC	TGT	GAG	TGC	CCA	GGC	624
Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly	
		195					200					205				
GAA	TTT	ATG	GGA	AGA	AAT	TGT	CAA	TAC	AAA	TGC	TCA	GGC	CCA	CTG	GGA	672
Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly	Pro	Leu	Gly	
	210					215					220					
ATT	GAA	GGT	GGA	ATT	ATA	TCA	AAC	CAG	CAA	ATC	ACA	GCT	TCC	TCT	ACT	720
Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala	Ser	Ser	Thr	
	225				230					235					240	
CAC	CGA	GCT	CTT	TTT	GGA	CTC	CAA	AAA	TGG	TAT	CCC	TAC	TAT	GCA	CGT	768
His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr	Tyr	Ala	Arg	
				245					250					255		
CTT	AAT	AAG	AAG	GGG	CTT	ATA	AAT	GCG	TGG	ACA	GCT	GCA	GAA	AAT	GAC	816
Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala	Glu	Asn	Asp	
			260					265					270			
AGA	TGG	AAG	CGG	TGG	ATT	CAG	ATA	AAT	TTG	CAA	AGA	AAA	ATG	AGA	GTT	864
Arg	Trp	Lys	Arg	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys	Met	Arg	Val	
		275					280					285				
ACT	GGT	GTG	ATT	ACC	CAA	GGG	GCC	AAG	AGG	ATT	GGA	AGC	CCA	GAG	TAT	912
Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	Ile	Gly	Ser	Pro	Glu	Tyr	
	290					295					300					
ATA	AAA	TTC	TAC	AAA	ATT	GCC	TAC	AGT	AAT	GAT	GGA	AAG	ACT	TGG	GCA	960
Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys	Thr	Trp	Ala	
	305				310					315					320	
ATG	TAC	AAA	GTG	AAA	GGC	ACC	AAT	GAA	GAC	ATG	GTG	TTT	CGT	GGA	AAC	1008
Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	Met	Val	Phe	Arg	Gly	Asn	
				325					330					335		
ATT	GAT	AAC	AAC	ACT	CCA	TAT	GCT	AAC	TCT	TTC	ACA	CCC	CCC	ATA	AAA	1056
Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro	Pro	Ile	Lys	
				340				345					350			
GCT	CAG	TAT	GTA	AGA	CTC	TAT	CCC	CAA	GTT	TGT	CGA	AGA	CAT	TGC	ACT	1104
Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val	Cys	Arg	Arg	His	Cys	Thr	
		355					360					365				
TTG	CGA	ATG	GAA	CTT	CTT	GGC	TGT	GAA	CTG	TCG	GGT	TGT	TCT	GAG	CCT	1152
Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	Ser	Gly	Cys	Ser	Glu	Pro	
	370					375						380				

CTG GGT ATG AAA TCA GGA CAT ATA CAA GAC TAT CAG ATC ACT GCC TCC Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr Ala Ser 385 390 395 400	1200
AGC ATC TTC AGA ACG CTC AAC ATG GAC ATG TTC ACT TGG GAA CCA AGG Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu Pro Arg 405 410 415	1248
AAA GCT CGG CTG GAC AAG CAA GGC AAA GTG AAT GCC TGG ACC TCT GGC Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr Ser Gly 420 425 430	1296
CAC AAT GAC CAG TCA CAA TGG TTA CAG GTG GAT CTT CTT GTT CCA ACC His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val Pro Thr 435 440 445	1344
AAA GTG ACT GGC ATC ATT ACA CAA GGA GCT AAA GAT TTT GGT CAT GTA Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly His Val 450 455 460	1392
CAG TTT GTT GGC TCC TAC AAA CTG GCT TAC AGC AAT GAT GGA GAA CAC Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly Glu His 465 470 475 480	1440
TGG ACT GTA TAC CAG GAT GAA AAG CAA AGA AAA GAT AAG GTT TTC CAG Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val Phe Gln 485 490 495	1488
GGA AAT TTT GAC AAT GAC ACT CAC AGA AAA AAT GTC ATC GAC CCT CCC Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp Pro Pro 500 505 510	1536
ATC TAT GCA CGA CAC ATA AGA ATC CTT CCT TGG TCC TGG TAC GGG AGG Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr Gly Arg 515 520 525	1584
ATC ACA TTG GCG TCA GAG CTG CTG GGC TGC ACA GAG GAG GAA TGA GGG Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu * Gly 530 535 540	1632
GAG GCT ACA TTT CAC AAC CGT CTT CCC TAT TTG GGT AAA AGT ATC TCC Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile Ser 545 550 555 560	1680
ATG GAA TGA ACT GTG TAA AAT CTG TAG GAA ACT GAA TGG TTT TTT TTT Met Glu * Thr Val * Asn Leu * Glu Thr Glu Trp Phe Phe Phe 565 570 575	1728
TTT TCA TGA AAA AGT GGT CAA ATT ATG GTA GGC AAC TAA CGG TGT TTT Phe Ser * Lys Ser Gly Gln Ile Met Val Gly Asn * Arg Cys Phe 580 585 590	1776
TAC C Tyr	1780

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Lys Arg Thr Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 517 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Leu * * Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser
1 5 10 15

Ala Thr Leu Pro Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro
20 25 30

Gly Asp Gly Ile Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly
35 40 45

Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro
50 55 60

Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly
65 70 75 80

Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser
85 90 95

Ser Val Val Glu Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly
100 105 110

Pro Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser
115 120 125

Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro
130 135 140

Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu
145 150 155 160

Val	Glu	Pro	Cys	Lys	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	
				165					170					175		
Tyr	Ser	Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	
			180					185				190				
Lys	Cys	Ser	Gly	Pro	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	
		195					200					205				
Gln	Ile	Thr	Ala	Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	
	210					215					220					
Trp	Tyr	Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	
225				230						235					240	
Trp	Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Lys	Arg	Trp	Ile	Gln	Ile	Asn	
				245					250					255		
Leu	Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	
			260					265					270			
Arg	Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	
		275					280					285				
Asn	Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	
	290					295					300					
Asp	Met	Val	Phe	Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	
305					310					315					320	
Ser	Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	
				325					330					335		
Val	Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	
			340					345					350			
Leu	Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	
		355					360					365				
Asp	Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	
	370					375					380					
Met	Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	
385					390					398					400	
Val	Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	
				405					410					415		
Val	Asp	Leu	Leu	Val	Pro	Thr	Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	
			420					425					430			
Ala	Lys	Asp	Phe	Gly	His	Val	Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	
		435					440					445				
Tyr	Ser	Asn	Asp	Gly	Glu	His	Trp	Thr	Val	Tyr	Gln	Asp	Glu	Lys	Gln	
	450					455					460					
Arg	Lys	Asp	Lys	Val	Phe	Gln	Gly	Asn	Phe	Asp	Asn	Asp	Thr	His	Arg	
465					470					475					480	
Lys	Asn	Val	Ile	Asp	Pro	Pro	Ile	Tyr	Ala	Arg	His	Ile	Arg	Ile	Leu	
				485					490					495		

Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly
500 505 510

Cys Thr Glu Glu Glu
515

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
1 5 10 15
Ser Met Glu * Thr Val * Asn Leu
20 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Glu Trp Phe Phe Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Gly Gln Ile Met Val Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Cys Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACAGATGGC CATGGATTCA GATAAATTG CAAAGAAAAA TGAGAGTCAC TGGTGTATT 60
ACCCAAGGAG CAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATTGCCTAC 120
AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAAG GCACCAATGA AGAGATGGTC 180
TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCCAATCAAA 240
GCTCAGTATG TAAGACTCTA CCCCCAAATT TGTCGAAGGC ATTGTACTTT AAGAATGGAA 300
CTTCTTGGCT GTGAGCTC 318

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
1 5 10 15
Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
20 25 30
Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
35 40 45
His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu
50 55 60
Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg
65 70 75 80
Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu
85 90 95

Asp	Gly	Xaa	Arg	Lys	Phe	Glu	Phe	Ile	Gln	Asp	Glu	Ser	Gly	Gly	Asp	100	105	110
Lys	Glu	Phe	Leu	Gly	Asn	Leu	Asp	Asn	Asn	Ser	Leu	Lys	Val	Asn	Met	115	120	125
Phe	Asn	Pro	Thr	Leu	Glu	Ala	Gln	Tyr	Ile	Arg	Leu	Tyr	Pro	Val	Ser	130	135	140
Cys	His	Arg	Gly	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu	Leu	145	150	155
His	Gly	Cys	Leu	Glu	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Thr	Ile	Pro	Asp	165	170	175
Ser	Gln	Met	Ser	Ala	Ser	Ser	Ser	Tyr	Lys	Thr	Trp	Asn	Leu	Arg	Ala	180	185	190
Phe	Gly	Trp	Tyr	Pro	His	Leu	Gly	Arg	Leu	Asp	Asn	Gln	Gly	Lys	Ile	195	200	205
Asn	Ala	Trp	Thr	Ala	Gln	Ser	Asn	Ser	Ala	Lys	Glu	Trp	Leu	Gln	Val	210	215	220
Asp	Leu	Gly	Thr	Gln	Arg	Gln	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	225	230	235
Arg	Asp	Phe	Gly	His	Ile	Gln	Tyr	Val	Glu	Ser	Tyr	Lys	Val	Ala	His	245	250	255
Ser	Asp	Asp	Gly	Val	Gln	Trp	Thr	Val	Tyr	Xaa	Xaa	Glu	Glu	Gln	Gly	260	265	270
Ser	Ser	Lys	Val	Phe	Gln	Gly	Asn	Leu	Asp	Asn	Asn	Ser	His	Lys	Lys	275	280	285
Asn	Ile	Phe	Glu	Lys	Pro	Phe	Met	Ala	Arg	Tyr	Val	Arg	Val	Leu	Pro	290	295	300
Val	Ser	Trp	His	Asn	Arg	Ile	Thr	Leu	Arg	Leu	Glu	Leu	Leu	Gly	Cys	305	310	315

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys	Ser	Gly	Pro	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	1	5	10	15
Ile	Thr	Ala	Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	20	25	30	

Tyr	Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp
	35						40					45			
Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Asn	Arg	Trp	Ile	Gln	Ile	Asn	Leu
	50					55					60				
Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg
65					70					75					80
Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn
				85					90					95	
Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp
			100					105					110		
Met	Val	Phe	Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser
		115					120					125			
Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val
	130					135					140				
Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu
145					150					155					160
Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp
				165					170					175	
Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met
			180					185					190		
Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val
		195					200					205			
Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val
	210					215					220				
Xaa	Leu	Leu	Val	Pro	Thr	Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala
225					230					235					240
Lys	Asp	Xaa	Gly	His	Val	Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	Tyr
				245					250					255	
Ser	Asn	Asp	Gly	Glu	His	Trp	Thr	Val	Xaa	Gln	Asp	Glu	Lys	Gln	Arg
			260					265					270		
Lys	Asp	Lys	Val	Xaa	Gln	Gly	Asn	Phe	Asp	Asn	Asp	Thr	His	Arg	Lys
		275					280					285			
Asn	Val	Ile	Asp	Pro	Pro	Ile	Tyr	Ala	Arg	His	Ile	Arg	Ile	Leu	Pro
	290					295					300				
Trp	Ser	Trp	Tyr	Gly	Arg	Ile	Thr	Leu	Ala	Ser	Glu	Leu	Leu	Gly	Cys
305					310					315					320
Thr															

(2) INFORMATION FOR SEQ ID NO:22:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15
Val Pro Gln Phe Gly Lys Gly Asp Ile
20 25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1 5 10 15
Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
20 25 30
Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
35 40 45
Glu Glu Glu Pro Thr Ser Ala Gly Pro
50 55

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1 5 10 15
Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
 1 5 10 15

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Tyr Ser Cys Glu Cys Pro Gly
 20 25 30

Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys
 35 40

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
 20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
 35 40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT	60
GTAGGTTTCCT TTTCCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAACCTG TTCTAGTGTT	120
GTGGAGGTTG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT	180
GAAGCATACC GAGGGGATAC ATTCATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT	240
GGGATTCACT GTCAGCACAA CATAAATGAA TGCGAAGTTG AGCCTTGCAA AAATGGTGGA	300
ATATGTACAG	310

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 549..1211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCGGG AGGGAGGGTA GGGGGGCGGG CCGCGGGGGG CCAAAGCCAG CTAGGCTCAG	60
TCTCACACGC GCGCCGCCAC TGTTTGATA TAGTGCGCTC CTGGCCTCAG GCTCGCTCCC	120
CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC	180
GTGAGCCGTA GTCAGTCTG GCGCTTCGC CTGCGTGCGC GCACGGAAAT CGGGGAGCCA	240
GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCCTCTGCT AGACCACTCG CAGCCCCAGC	300
CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA	360
ATCACCCCTT CTCTAGGGCC ACCACTCTTT TATCGCCCTT CCCAAGATTT GAGAAGCGCT	420
GCGGGAGGAA AGACGTCCTC TTGATCTCTG ACAGGGCGGG GTTACTGCT GTCCTGCAGG	480
CGCGCCTCGC CTAAGTGCC CTCCGCTACG ACCCGGACC AGCCAGGTC ACGTCCGTGA	540
GAAGGGATCA TGAAGCACTT GGTAGCAGCC TGGCTTTTGG TTGGACTCAG CCTCGGGGTG	600
CCCCAGTTCG GCAAAGGTGA CATTTGCAAC CCGAACCCT GTGAAAATGG TGGCATCTGT	660
CTGTCAGGAC TGGCTGATGA TTCCTTTTCC TGTGAGTGTC CAGAAGGCTT CGCAGGTCCG	720
AACTGCTCTA GTGTTGTGGA GGTGTCATCA GATGAAGAAA AGCCTACTTC AGCAGGTCCC	780
TGCATCCCTA ACCCATGCCA TAACGGAGGA ACCTGTGAGA TAAGCGAAGC CTATCGAGGA	840

GACACATTCA TAGGCTATGT TTGTAAATGT CCTCGGGGAT TTAATGGGAT TCACTGTCAG	900
CACAATATAA ATGAATGTGA AGCTGAGCCT TGCAGAAATG GCGGAATATG TACCGACCTT	960
GTTGCTAACT ACTCTTGTGA ATGCCCAGGA GAATTTATGG GACGAAATTG TCAATATAAA	1020
TGCTCTGGGC ACTTGGGAAT CGAAGGTGGG ATCATATCTA ATCAGCAAAT CACAGCTTCA	1080
TCTAATCACC GAGCTCTTTT TGGACTCCAG AAGTGGTATC CCTACTATGC TAGACTTAAT	1140
AAGAAGGGCC TTATAAATGC CTGGACAGCT GCTGAAAATG ACAGATGGCC ATGGATTCAG	1200
GTAACAGTGG GATGAGACAA ATCCATTTCC CAAATTATCA GAATCATTAT AGAAGTAGGT	1260
TAGGGAGAAT TGGCTGTGAT TCTTTCTCAT GGTTAAAATG TGATTTAGTT CAGAATTAAC	1320
ATGGTTGGAA ACTCTAAAAA ATGTGGAAAA CAGGAACATT CTATGTCTGA AAATCTGAAA	1380
ATAGCATCAA GATGAAAACA TTCTTTAGTC ATAAATATAC TCTTTTAAGT TATAGTAGAG	1440
AAAAAGATCT TATCATTTC AAGTGGACT TTTGGGATAG CATTGGAAAT GTAAATGAAA	1500
TAAATACCTA ATTGAAAAAA GTTTATTCTA AAGTGTTAAT ATTTAGCAAC AGATTCAGAG	1560
ACAAGAAAGT AACAATTCAA TCTGTGTATT TTTTGTGAGA AATAGTTTCC CATGTGCAAA	1620
TATAAAGTGC GCATCATATC ATGATAATAT CCAACTGTCT GCAGAACTCC CTTTCATAAA	1680
TGAGAGAATT TTAATTCATA GTGCCTTATA TCCTCATCAG CCATCTGACT TTAATACAGA	1740
AGAAAACAAT GAAATGATGC ATTAAGTGCT TTGCTAGAAG AAACATCATA GCAAAGCTGA	1800
TAGCCACAT TCTGTGCANN NAAGCTTCCA GAGCACTCGA GAAAAAGCAG AAATGAGATG	1860
TTTTATGAAA ACCGAAAAGA TAATCTGATT TCTGTGAAAT ATACTTTTGA TCATGTGGTT	1920
CTTTAAGATA GTCACCTACA AGTCATTAGT AGCAGATACC AAATGGGAGA AAATTTCCAG	1980
TATACTGAGG GTCAAGGCAG TCATGCTGAA ACTACATGAG GTCAGGAAAG TTTTGAAATA	2040
AGGTGATTTT GGAAGGATAC CTTCAACTGG CCTAGATTTT CAAGAAACAG TGTAATCAAC	2100
AGCCAAACAT GAGAATCTAG CTAACAGCAT TTAGAAAACC AGAACTAAGA GTGTTACTGG	2160
GGAATTGCAT TTAAATCCAG TATGAGAGTT TGCAAATGCC GTATTCTTCT AAGGGGTTTG	2220
TGCCACATTT TGTTACCATG GAGTCCTCTG TAAGAACTTT ATTAGATAAA TCATCTTTAC	2280
ACTATAATTT GAATAAAAGC CGGAATTC	2308

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Lys	Arg	Ser	Val	Ala	Val	Trp	Leu	Leu	Val	Gly	Leu	Ser	Leu	Gly
1				5				10						15	

Val	Pro	Gln	Phe	Gly	Lys	Gly	Asp	Ile	Cys	Asp	Pro	Asn	Pro	Cys	Glu	
			20					25					30			
Asn	Gly	Gly	Ile	Cys	Leu	Pro	Gly	Leu	Ala	Val	Gly	Ser	Phe	Ser	Cys	
		35					40					45				
Glu	Cys	Pro	Asp	Gly	Phe	Thr	Asp	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu	
	50					55					60					
Val	Ala	Ser	Asp	Glu	Glu	Glu	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Thr	Pro	
65					70					75					80	
Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg	
			85						90					95		
Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn	
			100					105					110			
Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Val	Glu	Pro	Cys	
		115					120					125				
Lys	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu	
	130					135						140				
Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly	
145					150					155					160	
Pro	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala	
				165					170					175		
Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr	
			180					185					190			
Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala	
		195					200					205				
Glu	Asn	Asp	Arg	Trp	Lys	Arg	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys	
	210					215					220					
Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	Ile	Gly	Ser	
225					230					235					240	
Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys	
				245					250					255		
Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	Met	Val	Phe	
			260					265					270			
Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro	
		275					280					285				
Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val	Cys	Arg	Arg	
	290					295					300					
His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	Ser	Gly	Cys	
305					310					315					320	
Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	Tyr	Gln	Ile	
				325					330					335		
Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	Phe	Thr	Trp	
			340					345					350			

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
 355 360 365
 Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Xaa Leu Leu
 370 375 380
 Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Xaa
 385 390 395 400
 Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
 405 410 415
 Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg Lys Asp Lys
 420 425 430
 Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
 435 440 445
 Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
 450 455 460
 Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
 465 470 475
 Glu
 480

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Quertermous, Thomas
Hogan, Brigid
Snodgrass, H. Ralph
Zupancic, Thomas J.

(ii) TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
CELL LOCUS-1

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/659,235
(B) FILING DATE: 05-JUN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Poissant, Brian M.
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-0034-899

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-8864/9741
(C) TELEX: 66141 Pennie

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15

Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
 20 25 30
 Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
 35 40 45
 Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
 50 55 60
 Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
 65 70 75 80
 Leu Pro Leu Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val
 20 25 30
 Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
 35 40 45
 Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
 50 55 60
 Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
 65 70 75 80
 Leu Pro Val Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Cys Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile
 20 25 30
 His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
 35 40 45
 Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
 50 55 60
 Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val
 65 70 75 80
 Ile Pro Lys Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Val Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile
 20 25 30
 Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
 35 40 45
 Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
 50 55 60
 Met Met Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
1 5 10 15
Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
20 25 30
Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
35 40 45
Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
50 55 60
Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
65 70 75 80
Arg Pro Val Thr Trp
85

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Xaa
1 5 10 15
Xaa Gly Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile
20 25 30
Gly Tyr Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser
35 40 45
Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
50 55 60
Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
65 70 75 80
Ile Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly	Cys	Glu	Val	Pro	Arg	Thr	Phe	Met	Cys	Val	Ala	Leu	Gln	Gly	Xaa
1				5				10					15		
Xaa	Xaa	Arg	Gly	Xaa	Asp	Ala	Asp	Gln	Trp	Val	Thr	Ser	Tyr	Lys	Ile
			20					25					30		
Arg	Tyr	Ser	Leu	Asp	Asn	Val	Ser	Trp	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Glu
		35					40					45			
Tyr	Arg	Asn	Gly	Ala	Ala	Ile	Thr	Gly	Val	Thr	Asp	Arg	Asn	Thr	Val
	50					55					60				
Val	Asn	His	Phe	Phe	Asp	Thr	Pro	Ile	Arg	Ala	Arg	Ser	Ile	Ala	Ile
65					70					75					80
His	Pro	Leu	Thr	Xaa											
				85											

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Xaa
1				5					10					15	
Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Val	Xaa	Ser	Tyr	Lys	Ile
			20					25					30		
Xaa	Tyr	Ser	Xaa	Asp	Gly	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40					45			
Xaa	Xaa	Lys	Xaa	Lys	Val	Phe	Xaa	Gly	Asn	Thr	Asp	Xaa	Xaa	Thr	Xaa
	50					55					60				
Xaa	Xaa	Asn	Xaa	Phe	Xaa	Xaa	Pro	Ile	Xaa	Xaa	Arg	Phe	Ile	Arg	Xaa
65					70					75					80
Xaa	Pro	Xaa	Xaa	Xaa											
				85											

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 619..2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAGTG ATATTTGATT TCCATTCTCA	60
TTCCCAGTGG CCTTGATATT TAAACTGATT CCTGCCACCA GGTCTTGGG CCACCCTGTC	120
CCTGCGTCTC ATATTTCTGC ATGCTGCTTT GTTGTATAT AGTGCGCTCC TGGCCTCAGG	180
CTCGTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCC GCATCCGCCG	240
CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TCGTGCGCG CACGGAAATC	300
GGGGAGCCAG GAACCAAGG AGCCGCCGTC CGCCGCTGT GCCTCTGCTA GACCACTCGC	360
AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG	420
TGAGGGTGAA TCACCCTTTC TCTAGGGCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTG	480
AGAAGCGCTG CGGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGGCGGGG TTTACTGCTG	540
TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCCAGGACCA GCCCAGGTCA	600
CGTCCGTGAG AAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT	651
Met Lys His Leu Val Ala Ala Trp Leu Leu Val	
1 5 10	
GGA CTC AGC CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC	699
Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn	
15 20 25	
CCG AAC CCC TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT	747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp	
30 35 40	
GAT TCC TTT TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC	795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys	
45 50 55	
TCT AGT GTT GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA	843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala	
60 65 70 75	
GGT CCC TGC ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA	891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile	
80 85 90	
AGC GAA GCC TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT	939
Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys	
95 100 105	
CCT CGG GGA TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT	987
Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys	
110 115 120	
GAA GCT GAG CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT	1035

Glu	Ala	Glu	Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala		
125						130					135						
AAC	TAC	TCT	TGT	GAA	TGC	CCA	GGA	GAA	TTT	ATG	GGA	CGA	AAT	TGT	CAA	1083	
Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	155	
140					145					150							
TAT	AAA	TGC	TCT	GGG	CAC	TTG	GGA	ATC	GAA	GGT	GGG	ATC	ATA	TCT	AAT	1131	
Tyr	Lys	Cys	Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	170	
				160					165								
CAG	CAA	ATC	ACA	GCT	TCA	TCT	AAT	CAC	CGA	GCT	CTT	TTT	GGA	CTC	CAG	1179	
Gln	Gln	Ile	Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	185	
			175					180									
AAG	TGG	TAT	CCC	TAC	TAT	GCT	CGA	CTT	AAT	AAG	AAG	GGC	CTT	ATA	AAT	1227	
Lys	Trp	Tyr	Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	200	
		190					195					200					
GCC	TGG	ACA	GCT	GCT	GAA	AAT	GAC	AGA	TGG	CCA	TGG	ATT	CAG	ATA	AAT	1275	
Ala	Trp	Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Ile	Asn	205	
	205					210					215						
TTG	CAA	AGA	AAA	ATG	AGA	GTC	ACT	GGT	GTT	ATT	ACC	CAA	GGA	GCA	AAA	1323	
Leu	Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	235	
220					225					230							
AGG	ATT	GGA	AGC	CCA	GAG	TAC	ATA	AAA	TCC	TAC	AAA	ATT	GCC	TAC	AGC	1371	
Arg	Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Ser	Tyr	Lys	Ile	Ala	Tyr	Ser	250	
				240					245								
AAT	GAC	GGG	AAG	ACC	TGG	GCA	ATG	TAC	AAA	GTA	AAA	GGC	ACC	AAT	GAA	1419	
Asn	Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	265	
			255				260						265				
GAG	ATG	GTC	TTT	CGT	GGA	AAT	GTT	GAT	AAC	AAC	ACA	CCA	TAT	GCT	AAT	1467	
Glu	Met	Val	Phe	Arg	Gly	Asn	Val	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	270	
		270				275						280					
TCT	TTC	ACA	CCC	CCA	ATC	AAA	GCT	CAG	TAT	GTA	AGA	CTC	TAC	CCC	CAA	1515	
Ser	Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	285	
		285				290					295						
ATT	TGT	CGA	AGG	CAT	TGT	ACT	TTA	AGA	ATG	GAA	CTT	CTT	GGC	TGT	GAG	1563	
Ile	Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	300	
300					305					310					315		
CTC	TCA	GGC	TGT	TCA	GAA	CCT	TTG	GGG	ATG	AAA	TCA	GGG	CAT	ATA	CAA	1611	
Leu	Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	320	
				320					325					330			
GAC	TAC	CAG	ATC	ACT	GCC	TCC	AGC	GTC	TTC	AGA	ACA	CTC	AAC	ATG	GAC	1659	
Asp	Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Val	Phe	Arg	Thr	Leu	Asn	Met	Asp	335	
			335					340					345				
ATG	TTT	ACT	TGG	GAA	CCA	AGG	AAA	GCC	AGG	CTG	GAC	AAG	CAA	GGC	AAA	1707	
Met	Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	350	
		350					355					360					
GTA	AAT	GCC	TGG	ACT	TCC	GGC	CAT	AAC	GAC	CAG	TCA	CAA	TGG	TTA	CAG	1755	
Val	Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	365	
						370					375						

GTT GAT CTT CTT GTC CCT ACT AAG GTG ACA GGC ATC ATT ACA CAA GGA	1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly	
380 385 390 395	
GCT AAA GAT TTT GGT CAC GTG CAG TTT GTT GGG TCA TAC AAA CTA GCT	1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala	
400 405 410	
TAC AGC AAT GAT GGA GAA CAC TGG ATG GTG CAC CAG GAT GAA AAA CAG	1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln	
415 420 425	
AGG AAA GAC AAG GTT TTT CAA GGC AAT TTT GAC AAT GAC ACT CAC AGG	1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg	
430 435 440	
AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA TTC ATA AGA ATC CTT	1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu	
445 450 455	
CCT TGG TCC TGG TAT GGA AGG ATC ACT CTG CGG TCA GAG CTG CTG GGC	2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly	
460 465 470 475	
TGC GCA GAG GAG GAA TGAAGTGCGG GGCCGCACAT CCCACAATGC TTTTCTTTAT	2098
Cys Ala Glu Glu Glu	
480	
TTTCCTATAA GTATCTCCAC GAAATGAACT GTGTGAAGCT GATGGAACT GCATTTGTTT	2158
TTTTCAAAGT GTTCAAATTA TGGTAGGCTA CTGACTGTCT TTTTAGGAGT TCTAAGCTTG	2218
CCTTTTAAAT AATTTAATTT GGTTTCCTTT GCTCAACTCT CTTATGTAAT ATCACACTGT	2278
CTGTGAGTTA CTCTTCTTGT TCTCT	2303

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15
Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30
Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45
Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60
Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg		
				85					90					95			
Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn		
			100					105					110				
Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Ala	Glu	Pro	Cys		
		115					120					125					
Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu		
	130					135					140						
Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly		
145					150					155					160		
His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala		
				165					170					175			
Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr		
			180					185					190				
Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala		
		195					200					205					
Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys	Met		
	210					215					220						
Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	Ile	Gly	Ser	Pro		
225					230					235					240		
Glu	Tyr	Ile	Lys	Ser	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys	Thr		
				245					250					255			
Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Glu	Met	Val	Phe	Arg		
			260					265					270				
Gly	Asn	Val	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro	Pro		
		275					280					285					
Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Ile	Cys	Arg	Arg	His		
	290					295					300						
Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	Ser	Gly	Cys	Ser		
305					310					315					320		
Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	Tyr	Gln	Ile	Thr		
				325					330					335			
Ala	Ser	Ser	Val	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	Phe	Thr	Trp	Glu		
			340					345					350				
Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val	Asn	Ala	Trp	Thr		
		355					360					365					
Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val	Asp	Leu	Leu	Val		
	370					375					380						
Pro	Thr	Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Lys	Asp	Phe	Gly		
385					390					395					400		
His	Val	Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	Tyr	Ser	Asn	Asp	Gly		
				405					410					415			

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445

Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460

Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCT CTT TAG TCA CCA CTC TCG CCC TCT CCA AGA ATT TGT TTA ACA AAG	48
Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys	
1 5 10 15	
CGC TGA GGA AAG AGA ACG TCT TCT TGA ATT CTT TAG TAG GGG CGG AGT	96
Arg * Gly Lys Arg Thr Ser Ser * Ile Leu * * Gly Arg Ser	
20 25 30	
CTG CTG CTG CCC TGC GCT GCC ACC TCG GCT ACA CTG CCC TCC GCG ACG	144
Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro Ser Ala Thr	
35 40 45	
ACC CCT GAC CAG CCG GGG TCA CGT CCG GGA GAC GGG ATC ATG AAG CGC	192
Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile Met Lys Arg	
50 55 60	
TCG GTA GCC GTC TGG CTC TTG GTC GGG CTC AGC CTC GGT GTC CCC CAG	240
Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly Val Pro Gln	
65 70 75 80	
TTC GGC AAA GGT GAT ATT TGT GAT CCC AAT CCA TGT GAA AAT GGA GGT	288
Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly	
85 90 95	
ATC TGT TTG CCA GGA TTG GCT GTA GGT TCC TTT TCC TGT GAG TGT CCA	336
Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro	
100 105 110	
GAT GGC TTC ACA GAC CCC AAC TGT TCT AGT GTT GTG GAG GTT GCA TCA	384
Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser	
115 120 125	

GAT Asp	GAA Glu	GAA Glu	GAA Glu	CCA Pro	ACT Thr	TCA Ser	GCA Ala	GGT Gly	CCC Pro	TGC Cys	ACT Thr	CCT Pro	AAT Asn	CCA Pro	TGC Cys	432
130						135					140					
CAT His	AAT Asn	GGA Gly	GGA Gly	ACC Thr	TGT Cys	GAA Glu	ATA Ile	AGT Ser	GAA Glu	GCA Ala	TAC Tyr	CGA Arg	GGG Gly	GAT Asp	ACA Thr	480
145					150					155					160	
TTC Phe	ATA Ile	GGC Gly	TAT Tyr	GTT Val	TGT Cys	AAA Lys	TGT Cys	CCC Pro	CGA Arg	GGA Gly	TTT Phe	AAT Asn	GGG Gly	ATT Ile	CAC His	528
				165					170					175		
TGT Cys	CAG Gln	CAC His	AAC Asn	ATA Ile	AAT Asn	GAA Glu	TGC Cys	GAA Glu	GTT Val	GAG Glu	CCT Pro	TGC Cys	AAA Lys	AAT Asn	GGT Gly	576
			180					185					190			
GGA Gly	ATA Ile	TGT Cys	ACA Thr	GAT Asp	CTT Leu	GTT Val	GCT Ala	AAC Asn	TAT Tyr	TCC Ser	TGT Cys	GAG Glu	TGC Cys	CCA Pro	GGC Gly	624
		195					200					205				
GAA Glu	TTT Phe	ATG Met	GGA Gly	AGA Arg	AAT Asn	TGT Cys	CAA Gln	TAC Tyr	AAA Lys	TGC Cys	TCA Ser	GGC Gly	CCA Pro	CTG Leu	GGA Gly	672
	210					215					220					
ATT Ile	GAA Glu	GGT Gly	GGA Gly	ATT Ile	ATA Ile	TCA Ser	AAC Asn	CAG Gln	CAA Gln	ATC Ile	ACA Thr	GCT Ala	TCC Ser	TCT Ser	ACT Thr	720
225					230					235					240	
CAC His	CGA Arg	GCT Ala	CTT Leu	TTT Phe	GGA Gly	CTC Leu	CAA Gln	AAA Lys	TGG Trp	TAT Tyr	CCC Pro	TAC Tyr	TAT Tyr	GCA Ala	CGT Arg	768
				245					250					255		
CTT Leu	AAT Asn	AAG Lys	AAG Lys	GGG Gly	CTT Leu	ATA Ile	AAT Asn	GCG Ala	TGG Trp	ACA Thr	GCT Ala	GCA Ala	GAA Glu	AAT Asn	GAC Asp	816
			260					265					270			
AGA Arg	TGG Trp	AAG Lys	CGG Arg	TGG Trp	ATT Ile	CAG Gln	ATA Ile	AAT Asn	TTG Leu	CAA Gln	AGA Arg	AAA Lys	ATG Met	AGA Arg	GTT Val	864
		275					280					285				
ACT Thr	GGT Gly	GTG Val	ATT Ile	ACC Thr	CAA Gln	GGG Gly	GCC Ala	AAG Lys	AGG Arg	ATT Ile	GGA Gly	AGC Ser	CCA Pro	GAG Glu	TAT Tyr	912
	290					295					300					
ATA Ile	AAA Lys	TTC Phe	TAC Tyr	AAA Lys	ATT Ile	GCC Ala	TAC Tyr	AGT Ser	AAT Asn	GAT Asp	GGA Gly	AAG Lys	ACT Thr	TGG Trp	GCA Ala	960
305					310					315					320	
ATG Met	TAC Tyr	AAA Lys	GTG Val	AAA Lys	GGC Gly	ACC Thr	AAT Asn	GAA Glu	GAC Asp	ATG Met	GTG Val	TTT Phe	CGT Arg	GGA Gly	AAC Asn	1008
				325					330					335		
ATT Ile	GAT Asp	AAC Asn	AAC Asn	ACT Thr	CCA Pro	TAT Tyr	GCT Ala	AAC Asn	TCT Ser	TTC Phe	ACA Thr	CCC Pro	CCC Pro	ATA Ile	AAA Lys	1056
				340				345					350			
GCT Ala	CAG Gln	TAT Tyr	GTA Val	AGA Arg	CTC Leu	TAT Tyr	CCC Pro	CAA Gln	GTT Val	TGT Cys	CGA Arg	AGA Arg	CAT His	TGC Cys	ACT Thr	1104
		355					360				365					
TTG Leu	CGA Arg	ATG Met	GAA Glu	CTT Leu	CTT Leu	GGC Gly	TGT Cys	GAA Glu	CTG Leu	TCG Ser	GGT Gly	TGT Cys	TCT Ser	GAG Glu	CCT Pro	1152
	370					375					380					

CTG	GGT	ATG	AAA	TCA	GGA	CAT	ATA	CAA	GAC	TAT	CAG	ATC	ACT	GCC	TCC	1200
Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	Tyr	Gln	Ile	Thr	Ala	Ser	
385					390				395						400	
AGC	ATC	TTC	AGA	ACG	CTC	AAC	ATG	GAC	ATG	TTC	ACT	TGG	GAA	CCA	AGG	1248
Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	Phe	Thr	Trp	Glu	Pro	Arg	
				405				410						415		
AAA	GCT	CGG	CTG	GAC	AAG	CAA	GGC	AAA	GTG	AAT	GCC	TGG	ACC	TCT	GGC	1296
Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val	Asn	Ala	Trp	Thr	Ser	Gly	
			420					425					430			
CAC	AAT	GAC	CAG	TCA	CAA	TGG	TTA	CAG	GTG	GAT	CTT	CTT	GTT	CCA	ACC	1344
His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val	Asp	Leu	Leu	Val	Pro	Thr	
		435				440						445				
AAA	GTG	ACT	GGC	ATC	ATT	ACA	CAA	GGA	GCT	AAA	GAT	TTT	GGT	CAT	GTA	1392
Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Lys	Asp	Phe	Gly	His	Val	
	450					455					460					
CAG	TTT	GTT	GGC	TCC	TAC	AAA	CTG	GCT	TAC	AGC	AAT	GAT	GGA	GAA	CAC	1440
Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	Tyr	Ser	Asn	Asp	Gly	Glu	His	
465					470					475					480	
TGG	ACT	GTA	TAC	CAG	GAT	GAA	AAG	CAA	AGA	AAA	GAT	AAG	GTT	TTC	CAG	1488
Trp	Thr	Val	Tyr	Gln	Asp	Glu	Lys	Gln	Arg	Lys	Asp	Lys	Val	Phe	Gln	
				485					490					495		
GGA	AAT	TTT	GAC	AAT	GAC	ACT	CAC	AGA	AAA	AAT	GTC	ATC	GAC	CCT	CCC	1536
Gly	Asn	Phe	Asp	Asn	Asp	Thr	His	Arg	Lys	Asn	Val	Ile	Asp	Pro	Pro	
			500					505					510			
ATC	TAT	GCA	CGA	CAC	ATA	AGA	ATC	CTT	CCT	TGG	TCC	TGG	TAC	GGG	AGG	1584
Ile	Tyr	Ala	Arg	His	Ile	Arg	Ile	Leu	Pro	Trp	Ser	Trp	Tyr	Gly	Arg	
		515					520					525				
ATC	ACA	TTG	GCG	TCA	GAG	CTG	CTG	GGC	TGC	ACA	GAG	GAG	GAA	TGA	GGG	1632
Ile	Thr	Leu	Ala	Ser	Glu	Leu	Leu	Gly	Cys	Thr	Glu	Glu	Glu	*	Gly	
	530					535					540					
GAG	GCT	ACA	TTT	CAC	AAC	CGT	CTT	CCC	TAT	TTG	GGT	AAA	AGT	ATC	TCC	1680
Glu	Ala	Thr	Phe	His	Asn	Arg	Leu	Pro	Tyr	Leu	Gly	Lys	Ser	Ile	Ser	
545					550					555					560	
ATG	GAA	TGA	ACT	GTG	TAA	AAT	CTG	TAG	GAA	ACT	GAA	TGG	TTT	TTT	TTT	1728
Met	Glu	*	Thr	Val	*	Asn	Leu	*	Glu	Thr	Glu	Trp	Phe	Phe	Phe	
				565					570					575		
TTT	TCA	TGA	AAA	AGT	GGT	CAA	ATT	ATG	GTA	GGC	AAC	TAA	CGG	TGT	TTT	1776
Phe	Ser	*	Lys	Ser	Gly	Gln	Ile	Met	Val	Gly	Asn	*	Arg	Cys	Phe	
			580					585					590			
TAC	C															1780
Tyr																

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys¹ Leu Thr Lys Arg
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Lys Arg Thr Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro
1 5 10 15

Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile
20 25 30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
35 40 45

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
50 55 60

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
65 70 75 80

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
85 90 95

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
100 105 110

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
115 120 125

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
130 135 140

Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Val	Glu	Pro	Cys	145	150	155	160
Lys	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu		165	170	175
Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly		180	185	190
Pro	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala		195	200	205
Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr	210	215	220	
Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala	225	230	235	240
Glu	Asn	Asp	Arg	Trp	Lys	Arg	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys		245	250	255
Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	Ile	Gly	Ser		260	265	270
Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys		275	280	285
Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	Met	Val	Phe	290	295	300	
Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro	305	310	315	320
Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val	Cys	Arg	Arg		325	330	335
His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	Ser	Gly	Cys		340	345	350
Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	Tyr	Gln	Ile		355	360	365
Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	Phe	Thr	Trp	370	375	380	
Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val	Asn	Ala	Trp	385	390	395	400
Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val	Asp	Leu	Leu		405	410	415
Val	Pro	Thr	Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Lys	Asp	Phe		420	425	430
Gly	His	Val	Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	Tyr	Ser	Asn	Asp		435	440	445
Gly	Glu	His	Trp	Thr	Val	Tyr	Gln	Asp	Glu	Lys	Gln	Arg	Lys	Asp	Lys	450	455	460	
Val	Phe	Gln	Gly	Asn	Phe	Asp	Asn	Asp	Thr	His	Arg	Lys	Asn	Val	Ile	465	470	475	480

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
 485 490 495

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
 500 505 510

Glu

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
 1 5 10 15

Ser Met Glu

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Glu Trp Phe Phe Phe Phe Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Gly Gln Ile Met Val Gly Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Cys Phe Tyr

1

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACAGATGGC CATGGATTCA GATAAATTTG CAAAGAAAAA TGAGAGTCAC TGGTGTATT 60
ACCCAAGGAG CAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATTGCCTAC 120
AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAAG GCACCAATGA AGAGATGGTC 180
TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCCAATCAAA 240
GCTCAGTATG TAAGACTCTA CCCCCTAATT TGTCTGAAGGC ATTGTACTTT AAGAATGGAA 300
CTTCTTGGCT GTGAGCTC 318

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
1 5 10 15
Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
20 25 30
Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
35 40 45
His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu
50 55 60
Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg
65 70 75 80
Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu

[illegible]

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
 1 5 10 15
 Val Pro Gln Phe Gly Lys Gly Asp Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
 1 5 10 15
 Ala Val Gly Xaa Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
 20 25 30
 Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
 35 40 45
 Glu Glu Glu Pro Thr Ser Ala Gly Pro
 50 55

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
 1 5 10 15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
1 5 10 15

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Tyr Ser Cys Glu Cys Pro Gly
20 25 30

Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys
35 40

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
35 40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT 60
GTAGGTTTCCT TTTCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAACCTG TTCTAGTGTT 120
GTGGAGGTTG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT 180
GAAGCATACC GAGGGGATAC ATTCATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT 240
GGGATTCACT GTCAGCACAA CATAAATGAA TCGAAGTTG AGCCTTGCAA AAATGGTGGA 300
ATATGTACAG 310

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 550...1212
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCGGG AGGGAGGGTA GGGGGGCGGG CCGCGGGGGC CCAAAGCCAG CTAGGCTCAG 60
TCTCACACGC GCGCCGCCAC TGTTTGTATA TAGTGCGCTC CTGGCCTCAG GCTCGCTCCC 120
CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC 180
GTGAGCCGTA GTCAGTCTG GCCGCTTCGC CTGCGTGCGC GCACGGAAAT CGGGGAGCCA 240
GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCCTCTGCT AGACCACTCG CAGCCCCAGC 300
CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA 360
ATCACCCCTT CTCTAGGGCC ACCACTCTTT TATCGCCCTT CCCAAGATTT GAGAAGCGCT 420
GCGGGAGGAA AGACGTCCTC TTGATCTCTG ACAGGGCGGG GTTTACTGCT GTCCTGCAGG 480
CGCGCCTCGC CTACTGTGCC CTCCGCTACG ACCCCGGACC AGCCCAGGTC ACGTCCGTGA 540
GAAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT GGA CTC AGC 591
Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser
1 5 10
CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC CCG AAC CCC 639
Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro
15 20 25 30

TGT	GAA	AAT	GGT	GGC	ATC	TGT	CTG	TCA	GGA	CTG	GCT	GAT	GAT	TCC	TTT	687
Cys	Glu	Asn	Gly	Gly	Ile	Cys	Leu	Ser	Gly	Leu	Ala	Asp	Asp	Ser	Phe	
			35						40					45		
TCC	TGT	GAG	TGT	CCA	GAA	GGC	TTC	GCA	GGT	CCG	AAC	TGC	TCT	AGT	GTT	735
Ser	Cys	Glu	Cys	Pro	Glu	Gly	Phe	Ala	Gly	Pro	Asn	Cys	Ser	Ser	Val	
			50					55					60			
GTG	GAG	GTT	GCA	TCA	GAT	GAA	GAA	AAG	CCT	ACT	TCA	GCA	GGT	CCC	TGC	783
Val	Glu	Val	Ala	Ser	Asp	Glu	Glu	Lys	Pro	Thr	Ser	Ala	Gly	Pro	Cys	
		65					70					75				
ATC	CCT	AAC	CCA	TGC	CAT	AAC	GGA	GGA	ACC	TGT	GAG	ATA	AGC	GAA	GCC	831
Ile	Pro	Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	
	80					85					90					
TAT	CGA	GGA	GAC	ACA	TTC	ATA	GGC	TAT	GTT	TGT	AAA	TGT	CCT	CGG	GGA	879
Tyr	Arg	Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	
95					100					105					110	
TTT	AAT	GGG	ATT	CAC	TGT	CAG	CAC	AAT	ATA	AAT	GAA	TGT	GAA	GCT	GAG	927
Phe	Asn	Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Ala	Glu	
				115					120					125		
CCT	TGC	AGA	AAT	GGC	GGA	ATA	TGT	ACC	GAC	CTT	GTT	GCT	AAC	TAC	TCT	975
Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	
			130					135					140			
TGT	GAA	TGC	CCA	GGA	GAA	TTT	ATG	GGA	CGA	AAT	TGT	CAA	TAT	AAA	TGC	1023
Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	
		145					150					155				
TCT	GGG	CAC	TTG	GGA	ATC	GAA	GGT	GGG	ATC	ATA	TCT	AAT	CAG	CAA	ATC	1071
Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	
	160					165					170					
ACA	GCT	TCA	TCT	AAT	CAC	CGA	GCT	CTT	TTT	GGA	CTC	CAG	AAG	TGG	TAT	1119
Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	
175					180					185					190	
CCC	TAC	TAT	GCT	AGA	CTT	AAT	AAG	AAG	GGC	CTT	ATA	AAT	GCC	TGG	ACA	1167
Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	
				195					200					205		
GCT	GCT	GAA	AAT	GAC	AGA	TGG	CCA	TGG	ATT	CAG	GTA	ACA	GTG	GGA	TGAGA	1217
Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Val	Thr	Val	Gly		
		210						215					220			
CAAATCCATT	TCCCAAATTA	TCAGAATCAT	TATAGAAGTA	GGTTAGGGAG	AATTGGCTGT											1277
GATTCTTTCT	CATGGTTAAA	ATGTGATTTA	G TTCAGAATT	AACATGGTTG	GAAACTCTAA											1337
AAAATGTGGA	AAACAGGAAC	ATTCTATGTC	TGAAAATCTG	AAAATAGCAT	CAAGATGAAA											1397
ACATTCTTTA	GTCATAAATA	TACTCTTTTA	AGTTATAGTA	GAGAAAAAGA	TCTTATCATT											1457
TCATAAGTGG	ACTTTTGGGA	TAGCATTGGA	AATGTAAATG	AAATAAATAC	CTAATTGAAA											1517
AAAGTTTATT	CTAAAGTGTT	AATATTTAGC	AACAGATTCA	GAGACAAGAA	AGTAACAATT											1577
CAATCTGTGT	ATTTTTTGTG	AGAAATAGTT	TCCCATGTGC	AAATATAAAG	TGCGCATCAT											1637
ATCATGATAA	TATCCAAC TG	TCTGCAGAAC	TCCCTTTTCAT	AAATGAGAGA	ATTTTAATTC											1697

ATAGTGCCTT ATATCCTCAT CAGCCATCTG ACTTTACTAC AGAAGAAAAC AATGAAATGA 1757
 TGCATTAAGT GCTTTGCTAG AAGAAACATC ATAGCAAAGC TGATAGCCCA CATTCTGTGC 1817
 ANNNAAGCTT CCAGAGCACT CGAGAAAAAG CAGAAATGAG 'ATGTTTTATG AAAACCGAAA 1877
 AGATAATCTG ATTTCTGTGA AATATACTTT TGATCATGTG GTTCTTTAAG ATAGTCACTA 1937
 ACAAGTCATT AGTAGCAGAT ACCAAATGGG AGAAAATTTT CAGTATACTG AGGGTCAAGG 1997
 CAGTCATGCT GAAACTACAT GAGGTCAGGA AAGTTTTGAA ATAAGGTGAT TTTGGAAGGA 2057
 TACCTTCAAC TGGCCTAGAT TTTCAAGAAA CAGTGTAATC AACAGCCAAA CATGAGAATC 2117
 TAGCTAACAG CATTTAGAAA ACCAGAACTA AGAGTGTTAC TGGGGAATTG CATTTAATC 2177
 CAGTATGAGA GTTTGCAAAT GCCGTATTCT TCTAAGGGGT TTGTGCCACA TTTTGTTACC 2237
 ATGGAGTCCT CTGTAAGAAC TTTATTAGAT AAATCATCTT TACACTATAA TTTGAATAAA 2297
 AGCCGGAATT C 2308

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Lys	His	Leu	Val	Ala	Ala	Trp	Leu	Leu	Val	Gly	Leu	Ser	Leu	Gly	1	5	10	15
Val	Pro	Gln	Phe	Gly	Lys	Gly	Asp	Ile	Cys	Asn	Pro	Asn	Pro	Cys	Glu	20	25	30	
Asn	Gly	Gly	Ile	Cys	Leu	Ser	Gly	Leu	Ala	Asp	Asp	Ser	Phe	Ser	Cys	35	40	45	
Glu	Cys	Pro	Glu	Gly	Phe	Ala	Gly	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu	50	55	60	
Val	Ala	Ser	Asp	Glu	Glu	Lys	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Ile	Pro	65	70	75	80
Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg	85	90	95	
Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn	100	105	110	
Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Ala	Glu	Pro	Cys	115	120	125	
Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu	130	135	140	
Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly				

145					150					155				160
His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr
				165					170				175	Ala
Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro
			180					185					190	Tyr
Tyr	Ala	Ala	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala
		195					200					205		Ala
Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Val	Thr	Val	Gly		
	210					215					220			

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